

SEQUENCE LISTING

<110> Consiglio Nazionale delle Ricerche

5 <120> Fusion proteins
 <130> BW352R
 <160> 7
 <170> PatentIn version 3.2

10 <210> 1
 <211> 732
 <212> DNA
 <213> Parietaria judaica
 <222> (1)..(729)

15 <220>
 <221> misc_feature
 <222> (10)..(12); (40)..(42); (85)..(90); (148)..(150); (154)..(156);
 (271)..(273); (322)..(324); (352)..(354); (397)..(402); (460)..(462);
 20 (466)..(468); (535)..(537); (583)..(585)
 <223> n is a, c, g, or t
 <400> 1

25 gag gag gct nnn ggg aaa gtg gtg cag gat ata atg ccg nnn ctg cat 48
 Glu Glu Ala Xaa Gly Lys Val Val Gln Asp Ile Met Pro Xaa Leu His
 1 5 10 15

30 ttc gtg aag ggg gag gag aag gag ccg tcg aag gag nnn nnn agc ggc 96
 Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Xaa Xaa Ser Gly
 20 25 30

35 acg aag aag ctg agc gag gag gtg aag acg acg gag cag aag agg gag 144
 Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu
 35 40 45

gcc nnn aag nnn ata gtg cgc gcc acg aag ggc atc tcc ggt atc aaa 192
 Ala Xaa Lys Xaa Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys
 50 55 60

40 aat gaa ctt gtc gcc gag gtc ccc aag aag nnn gat att aag acc act 240
 Asn Glu Leu Val Ala Glu Val Pro Lys Lys Xaa Asp Ile Lys Thr Thr
 65 70 75 80

45 ctc ccg ccc atc acc gcc gac ttc gac tgc nnn aag atc caa agt act 288
 Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Xaa Lys Ile Gln Ser Thr
 85 90 95

att ttc aga ggt tac tat gga ttc caa gaa acc nnn ggg act atg gtg 336
 Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Xaa Gly Thr Met Val
 100 105 110

50

aga gcg ctg atg ccg nnn ctg ccg ttc gtg cag ggg aaa gag aaa gag 384
 Arg Ala Leu Met Pro Xaa Leu Pro Phe Val Gln Gly Lys Glu Lys Glu
 115 120 125

5 ccg tca aag ggg nnn nnn agc ggc gcc aaa aga ttg gac ggg gag acg 432
 Pro Ser Lys Gly Xaa Xaa Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr
 130 135 140

10 aag acg ggg ccg cag agg gtg cac gct nnn gag nnn atc cag acc gcc 480
 Lys Thr Gly Pro Gln Arg Val His Ala Xaa Glu Xaa Ile Gln Thr Ala
 145 150 155 160

15 atg aag act tat tcc gac atc gac ggg aaa ctc gtc agc gag gtc ccc 528
 Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro
 165 170 175

aag cac nnn ggc atc gtt gac agc aag ctc ccg ccc att gac gtc aac 576
 Lys His Xaa Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn
 180 185 190

20 atg gac nnn aag aca gtt gga gtg gtt cct cgg caa ccc caa ctt cca 624
 Met Asp Xaa Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro
 195 200 205

25 gtc tct ctc cgt cat ggt ccc gtc acg ggc cca agt gat ccc gcc cac 672
 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His
 210 215 220

30 aaa gca cgg ttg gag aga ccc cag att aga gtt ccg ccc ccc gca ccg 720
 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro
 225 230 235 240

gaa aaa gcc taa 732
 Glu Lys Ala

35

40 <210> 2
 <211> 243
 <212> PRT
 <213> Parietaria judaica

45 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The 'Xaa' at location 4, 14, 29, 30, 50, 52, 75, 91, 108, 118, 133,
 154, 156, 179, 195 stands for Asn, Ser, Thr, Ile, Met, Gly, Ala, Val, Gln or
 Leu.

50 <400> 2

Glu Glu Ala Xaa Gly Lys Val Val Gln Asp Ile Met Pro Xaa Leu His
 1 5 10 15
 5 Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Xaa Xaa Ser Gly
 20 25 30
 Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu
 35 40 45
 10 Ala Xaa Lys Xaa Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys
 50 55 60
 Asn Glu Leu Val Ala Glu Val Pro Lys Lys Xaa Asp Ile Lys Thr Thr
 15 65 70 75 80
 Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Xaa Lys Ile Gln Ser Thr
 85 90 95
 20 Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Xaa Gly Thr Met Val
 100 105 110
 Arg Ala Leu Met Pro Xaa Leu Pro Phe Val Gln Gly Lys Glu Lys Glu
 115 120 125
 25 Pro Ser Lys Gly Xaa Xaa Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr
 130 135 140
 Lys Thr Gly Pro Gln Arg Val His Ala Xaa Glu Xaa Ile Gln Thr Ala
 30 145 150 155 160
 Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro
 165 170 175
 35 Lys His Xaa Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn
 180 185 190
 Met Asp Xaa Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro
 40 195 200 205
 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His
 210 215 220
 45 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro
 225 230 235 240
 Glu Lys Ala
 50

<210> 3
 <211> 732
 <212> DNA
 <213> Parietaria judaica
 5 <221> CDS
 <222> (1)..(729)

<400> 3

10 gag gag gct agc ggg aaa gtg gtg cag gat ata atg ccg tgc ctg cat 48
 Glu Glu Ala Ser Gly Lys Val Val Gln Asp Ile Met Pro Cys Leu His
 1 5 10 15

15 ttc gtg aag ggg gag gag aag gag ccg tgc aag gag agc agc agc ggc 96
 Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Ser Ser Ser Gly
 20 25 30

20 acg aag aag ctg agc gag gag gtg aag acg acg gag cag aag agg gag 144
 Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu
 35 40 45

25 gcc tgc aag tgc ata gtg cgc gcc acg aag ggc atc tcc ggt atc aaa 192
 Ala Cys Lys Cys Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys
 50 55 60

aat gaa ctt gtc gcc gag gtc ccc aag aag tgc gat att aag acc act 240
 Asn Glu Leu Val Ala Glu Val Pro Lys Lys Cys Asp Ile Lys Thr Thr
 65 70 75 80

30 ctc ccg ccc atc acc gcc gac ttc gac tgc tcc aag atc caa agt act 288
 Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Ser Lys Ile Gln Ser Thr
 85 90 95

35 att ttc aga ggt tac tat gga ttc caa gaa acc agc ggg act atg gtg 336
 Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Ser Gly Thr Met Val
 100 105 110

40 aga gcg ctg atg ccg tgc ctg ccg ttc gtg cag ggg aaa gag aaa gag 384
 Arg Ala Leu Met Pro Cys Leu Pro Phe Val Gln Gly Lys Glu Lys Glu
 115 120 125

45 ccg tca aag ggg agc agc agc ggc gcc aaa aga ttg gac ggg gag acg 432
 Pro Ser Lys Gly Ser Ser Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr
 130 135 140

aag acg ggg ccg cag agg gtg cac gct tgt gag tgc atc cag acc gcc 480
 Lys Thr Gly Pro Gln Arg Val His Ala Cys Glu Cys Ile Gln Thr Ala
 145 150 155 160

50 atg aag act tat tcc gac atc gac ggg aaa ctc gtc agc gag gtc ccc 528
 Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro
 165 170 175

aag cac tgc ggc atc gtt gac agc aag ctc ccg ccc att gac gtc aac 576
 Lys His Cys Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn
 180 185 190

5

atg gac tgc aag aca gtt gga gtg gtt cct cgg caa ccc caa ctt cca 624
 Met Asp Cys Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro
 195 200 205

10

gtc tct ctc cgt cat ggt ccc gtc acg ggc cca agt gat ccc gcc cac 672
 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His
 210 215 220

15

aaa gca cgg ttg gag aga ccc cag att aga gtt ccg ccc ccc gca ccg 720
 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro
 225 230 235 240

20

gaa aaa gcc taa 732
 Glu Lys Ala

25

<210> 4
 <211> 243
 <212> PRT
 <213> Parietaria judaica

30

Glu Glu Ala Ser Gly Lys Val Val Gln Asp Ile Met Pro Cys Leu His
 1 5 10 15

Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Ser Ser Ser Gly
 20 25 30

35

Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu
 35 40 45

40

Ala Cys Lys Cys Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys
 50 55 60

Asn Glu Leu Val Ala Glu Val Pro Lys Lys Cys Asp Ile Lys Thr Thr
 65 70 75 80

45

Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Ser Lys Ile Gln Ser Thr
 85 90 95

Ile Phe Arg Gly Tyr Tyr Gly-Phe Gln Glu Thr Ser Gly Thr Met Val
 100 105 110

50

Arg Ala Leu Met Pro Cys Leu Pro Phe Val Gln Gly Lys Glu Lys Glu
 115 120 125

Pro Ser Lys Gly Ser Ser Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr
 130 135 140

5 Lys Thr Gly Pro Gln Arg Val His Ala Cys Glu Cys Ile Gln Thr Ala
 145 150 155 160

Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro
 165 170 175

10 Lys His Cys Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn
 180 185 190

Met Asp Cys Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro
 195 200 205

15 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His
 210 215 220

20 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro
 225 230 235 240

Glu Lys Ala

25 <210> 5
 <211> 18
 <212> DNA
 <213> Artificial

30 <220>
 <223> forward primer for insertion of mutation in position 29 and 30

<400> 5
 gagagcagca gcggcagc 18

35 <210> 6
 <211> 30
 <212> DNA
 <213> Artificial

40 <220>
 <223> forward primer for insertion of mutation in position 4

<400> 6
 45 gtgggatccg aggaggctag cgggaaagtg 30

<210> 7
 <211> 24
 <212> DNA
 50 <213> Artificial

<220>

<223> reverse parj2 primer

<400> 7

5 gggggatcca tagtaacctc tgaa

24